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CanCore version 5.1.6
cm protein - protein search, using sw model
Run on: November 17, 2004, 14:59:59 / Search time 103.667 seconds
Title: US-10-705-716a-2
Perfect score: 767
Sequence: I MGCTGSRADAIERYVHSWT.....VTKNIKDRDKSKEVWTCIN 145
Scoring table: BLOSUM62
Gappen 10.0 , Gapext 0.5
Searched: 1825181 seqs, 575374646 residues

Total number of bits satisfying chosen parameters: 1825181

Maximum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first: 45 summaries

32 83.5 10.9 700 2 030678 xanthomonas
33 63.5 10.9 751 1 CNT03 MOUSE
34 63 10.8 561 2 0898F1 Obelia bradyrhizob
35 63 10.8 581 2 P89204 P89204 sugarcane m
36 63 10.8 1433 1 CAT8 YEAST pJ9113 saccharomyces
37 82.5 10.8 514 2 Q788F2 Q788F2 neurospora
38 82.5 10.8 853 1 AOP2 MOUSE Q6Q8B8 mus musculus
39 82.5 10.8 879 2 BAC97980 Bac97980 mus musculu
40 82.5 10.8 1597 2 Q6XK0 Q6XK0 streptomyce
41 82 10.7 339 2 Q8KRS5 Q8KRS5 streptomyce
42 82 10.7 882 1 ARBA ASPNG O13412 aspergillus
43 82 10.7 882 2 Q8H815 Q8H815 aspergill
44 82 10.7 1449 2 Q7XPE1 Q7XPE1 OTYRA sativ
45 81.5 10.6 397 2 Q94KA7 Q94KA7 phaseolus v

ALIGNMENTS

RESULT 1

0920KS ID PRELIMINARY, PRT, 145 AA.
Q920KS AC
DT 01-DBC-2001 (TREMBL; 19, Created)
DT 01-DBC-2004 (TREMBL; 19, Last sequence update)
DT 05-JUL-2004 (TREMBL; 27, Last annotation update)
DB Dm-A20-4 (BASIC isoform 1-6-8).
GN Name-A20-4; Synonyms-Basic;
OS Rattus norvegicus (Rat).
OC Bivalvia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Rutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1] NCBI_TaxId-10115;
RP SOURCE FROM N.A.
RA Wang X., Tian Q., Li W., Okano A., Suzuki T.,
RN Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.
[2] SOURCE FROM N.A.
RP SOURCE FROM N.A.
RC STRAIN=SPRague-Dawley/
RX MEDLINE=21574584, PubMed=11707601;

Result No. Score Query Match Length DB ID Description

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

2	0920K5	0920bs retus noto
2	0920V1	0920v1 mus musculus
2	09HMSJ	09hmsj homo sapiens
2	08HMS9	08hms9 sus scrofa
2	08HMS9	08hms9 homo sapiens
2	08HMS1	08hms1 homo sapiens
2	09Y03	09y03 mus musculus
2	09Y03	09y03 rattus rattus
2	08YB8	08yb8 mus musculus
2	08WKS0	08wks0 homo sapiens
2	08WTP5	08wt5 homo sapiens
2	AH35039	AH35039 homo sapiens
2	Q8W8Z	Q8w8z homo sapiens
2	Q8WTEB	Q8wteb sus scrofa
2	Q8Y015	Q8y015 brachyrhynchus
2	Q8ZP6	Q8zp6 homo sapiens
2	BAD18729	BAD18729 homo sapiens
1	CNOJ_HUMAN	CNOJ_HUMAN
1	PYD2_EUROPEAN	PYD2_EUROPEAN
1	Q0M020	Q0m020
1	P01284	P01284
3	Q76C74	Q76c74 saccharomyces
2	BAD05177	BAD05177 saccharomyces
2	OPT0B1	OPT0B1
2	BAD0676	BAD0676
2	Q7U229	Q7u229 baccharomyces
1	PYD2_PLAKT	PYD2_PLAKT
2	Q968L2	Q968l2 homo sapiens
2	Q8U5F5	Q8u5f5 plasmidium
2	AHQ92395	AHQ92395 plasmidium
2	Q8MC2	Q8mc2 leucosticha

RA	Mrozek K., Bill R., Koufos S., Kolitz J.B., Fletcher K.J.,
RA	Caligiuri M.A., Bloomfield C.D., de la Chapelle A.,
RT	BALMC, the human member of a novel mammalian neuroectoderm gene
RT	lineage, is implicated in hematopoiesis and acute leukaemia.
RL	Proc. Natl. Acad. Sci. U.S.A. 98:13901-13906 (2001).
DR	EML3: AB073131; BAB70507_1; ..
DR	EMBL: AP371311; ALUS0317..;
DR	InteliPRO; IPK009728; BALMC_N..
DR	PRF06989; PR06989;
SO	SEQUENCE .145 AA; 15475 MM; D5A27AD67456P341 CRC64;
	Query Match 100.0%; Score 767; DB 2; Length 145;
	Best Local Similarity 100.0%; Pred. No. 3.4e-61;
	Matches 145; Conservative 0; Mis.matches 0; Indels 0; Gaps 0;
Qy	MGCGGSRADAIERRPPRYSWTRTSTWTTTDSALPAHAAATSGPAGGGAGVARDGP 60
Db	1 MGCGGSRADAIERRPPRYSWTRTSTWTTTDSALPAHAAATSGPAGGGAGVARDGP 60
Qy	61 SSGNGLRDPAPGQIANPDKNGCCTGOCPPNSQSLASGPAKTKONGLMTBAKGDAKOMSAR 120
Db	61 SSGNGLRDPAPGQIANPDKNGCCTGOCPPNSQSLASGPAKTKONGLMTBAKGDAKOMSAR 120
Qy	121 RHALSVTENIROMDRKRTYTCIN 145
Db	121 EVASVTEVNIRDMDRKRTYTCIN 145
RESULT 2	
OBVIEW	
ID	OBVIEW, PRELIMINARY, PRT: 145 AA.
ORIGIN	

1	767	100.0	14
2	746	97.3	14
3	655	84.1	14
4	634	82.7	14
5	617.5	80.5	18
6	473.5	61.7	14
7	59.8	12.6	14
8	294	38.3	5
9	288	37.5	7
10	278	36.2	5
11	277	35.5	6
12	277	34.8	5
13	272	34.0	3
14	267	32.1	6
15	161	21.0	6
16	92.5	12.1	6
17	92.5	12.1	6
18	92.5	12.1	7
19	92.5	12.1	10
20	89.5	11.7	17
21	88	11.5	36
22	87	11.3	10
23	87	11.3	10
24	87	11.3	17
25	87	11.3	17
26	86	11.2	58
27	86	11.2	10
28	84.5	11.0	53
29	84	11.0	155
30	84	11.0	214
31	83.5	10.9	

